

<110> APPLICANT: Voellmy, Richard
 <120> TITLE OF INVENTION: MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
 SUSTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS
 <130> FILE REFERENCE: 870109.409
 <140> CURRENT APPLICATION NUMBER: US/10/046,420
 <141> CURRENT FILING DATE: 2002-04-19
 <150> PRIOR APPLICATION NUMBER: US/09/304,121
 <151> PRIOR FILING DATE: 1999-05-03
 <160> NUMBER OF SEQ ID NOS: 3
 <170> SOFTWARE: FastSEQ for Windows Version 3.0

<210> SEQ ID NO 1
 <211> LENGTH: 2156
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (161)...(1747)
 <400> SEQUENCE: 1

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gcggcgccgc ggcccgaag gctggcgcg cgacggcggtt agcccggccc tcggccctc      120
tttgcgcccg ctccctccgc ctattccctc cttgctcgag atg gat ctg ccc gtg      175
                               Met Asp Leu Pro Val
                               1           5

ggc ccc ggc gcg gcg ggg ccc agc aac gtc ccg gcc ttc ctg acc aag      223
Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe Leu Thr Lys
                               10           15           20

ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc atc tgc tgg      271
Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu Ile Cys Trp
                               25           30           35

agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc cag ttt gcc      319
Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly Gln Phe Ala
                               40           45           50

aag gag gtg ctg ccc aag tac ttc aag cac aac aac atg gcc agc ttc      367
Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser Phe
                               55           60           65

gtg cgg cag ctc aac atg tat ggc ttc cgg aaa gtg gtc cac atc gag      415
Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile Glu
                               70           75           80           85

cag ggc ggc ctg gtc aag cca gag aga gac acg gag ttc cag cac      463
Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu Phe Gln His
                               90           95           100

cca tgc ttc ctg cgt ggc cag gag cag ctc ctt gag aac atc aag agg      511
Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn Ile Lys Arg
                               105           110           115

aaa gtg acc agt gtg tcc acc ctg aag agt gaa gac ata aag atc cgc      559
Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile Lys Ile Arg
                               120           125           130

cag gac agc gtc acc aag ctg ctg acg gac gtg cag ctg atg aag ggg      607
Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val Gln Leu Met Lys Gly
                               135           140           145

aag cag gag tgc atg gac tcc aag ctc ctg gcc atg aag cat gag aat      655
Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala Met Lys His Glu Asn
                               150           155           160           165

gag gct ctg tgg cgg gag gtg gcc agc ctt cgg cag aag cat gcc cag      703
Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg Gln Lys His Ala Gln
                               170           175           180

caa cag aaa gtc gtc aac aag ctc att cag ttc ctg atc tca ctg gtg      751
Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe Leu Ile Ser Leu Val
                               185           190           195

cag tca aac cgg atc ctg ggg gtg aag aga aag atc ccc ctg atg ctg      799
Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys Ile Pro Leu Met Leu
                               200           205           210

aac gac agt ggc tca gca cat tcc atg ccc aag tat agc cgg cag ttc      847
Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys Tyr Ser Arg Gln Phe
  
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215	tcc	ctg	gag	cac	gtc	cac	ggc	tcg	ggc	ccc	tac	tcg	gcc	ccc	tcc	cca	895
	Ser	Leu	Glu	His	Val	His	Gly	Ser	Gly	Pro	Tyr	Ser	Ala	Pro	Ser	Pro	
230	gcc	tac	agc	agc	tcc	agc	ctc	tac	gcc	cct	gat	gct	gtg	gcc	agc	tct	943
	Ala	Tyr	Ser	Ser	Ser	Ser	Leu	Tyr	Ala	Pro	Asp	Ala	Val	Ala	Ser	Ser	
250	gga	ccc	atc	atc	tcc	gac	atc	acc	gag	ctg	gct	cct	gcc	agc	ccc	atg	991
	Gly	Pro	Ile	Ile	Ser	Asp	Ile	Thr	Glu	Leu	Ala	Pro	Ala	Ser	Pro	Met	
265	gcc	tcc	ccc	ggc	ggg	agc	ata	gac	gag	agg	ccc	cta	tcc	agc	agc	ccc	1039
	Ala	Ser	Pro	Gly	Gly	Ser	Ile	Asp	Glu	Arg	Pro	Leu	Ser	Ser	Ser	Pro	
280	ctg	gtg	cgt	gtc	aag	gag	gag	ccc	ccc	agc	ccg	cct	cag	agc	ccc	cgg	1087
	Leu	Val	Arg	Val	Lys	Glu	Glu	Pro	Pro	Ser	Pro	Pro	Gln	Ser	Pro	Arg	
295	gta	gag	gag	gcg	agt	ccc	ggg	cgc	cca	tct	tcc	gtg	gac	acc	ctc	ttg	1135
	Val	Glu	Glu	Ala	Ser	Pro	Gly	Arg	Pro	Ser	Ser	Val	Asp	Thr	Leu	Leu	
310	tcc	ccg	acc	gcc	ctc	att	gac	tcc	atc	ctg	cgg	gag	agt	gaa	cct	gcc	1183
	Ser	Pro	Thr	Ala	Leu	Ile	Asp	Ser	Ile	Leu	Arg	Glu	Ser	Glu	Pro	Ala	
330	ccc	gcc	tcc	gtc	aca	gcc	ctc	acg	gac	gcc	agg	ggc	cac	acg	gac	acc	1231
	Pro	Ala	Ser	Val	Thr	Ala	Leu	Thr	Asp	Ala	Arg	Gly	His	Thr	Asp	Thr	
345	gag	ggc	cgg	cct	ccc	tcc	ccc	ccg	ccc	acc	tcc	acc	cct	gaa	aag	tgc	1279
	Glu	Gly	Arg	Pro	Pro	Ser	Pro	Pro	Pro	Thr	Ser	Thr	Pro	Glu	Lys	Cys	
360	ctc	agc	gta	gcc	tgc	ctg	gac	aag	aat	gag	ctc	agt	gac	cac	ttg	gat	1327
	Leu	Ser	Val	Ala	Cys	Leu	Asp	Lys	Asn	Glu	Leu	Ser	Asp	His	Leu	Asp	
375	gct	atg	gac	tcc	aac	ctg	gat	aac	ctg	cag	acc	atg	ctg	agc	agc	cac	1375
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390	ggc	ttc	agc	gtg	gac	acc	agt	gcc	ctg	ctg	gac	ctg	ttc	agc	ccc	tcg	1423
	Gly	Phe	Ser	Val	Asp	Thr	Ser	Ala	Leu	Leu	Asp	Leu	Phe	Ser	Pro	Ser	
410	gtg	acc	gtg	ccc	gac	atg	agc	ctg	cct	gac	ctt	gac	agc	agc	ctg	gcc	1471
	Val	Thr	Val	Pro	Asp	Met	Ser	Leu	Pro	Asp	Leu	Asp	Ser	Ser	Leu	Ala	
425	agt	atc	caa	gag	ctc	ctg	tct	ccc	cag	gag	ccc	ccc	agg	cct	ccc	gag	1519
	Ser	Ile	Gln	Glu	Leu	Leu	Ser	Pro	Gln	Glu	Pro	Pro	Arg	Pro	Pro	Glu	
440	gca	gag	aac	agc	agc	ccg	gat	tca	ggg	aag	cag	ctg	gtg	cac	tac	aca	1567
	Ala	Glu	Asn	Ser	Ser	Pro	Asp	Ser	Gly	Lys	Gln	Leu	Val	His	Tyr	Thr	
455	gcg	cag	ccg	ctg	ttc	ctg	ctg	gac	ccc	ggc	tcc	gtg	gac	acc	ggg	agc	1615
	Ala	Gln	Pro	Leu	Phe	Leu	Leu	Asp	Pro	Gly	Ser	Val	Asp	Thr	Gly	Ser	
470	aac	gac	ctg	ccg	gtg	ctg	ttt	gag	ctg	gga	gag	ggc	tcc	tac	ttc	tcc	1663
	Asn	Asp	Leu	Pro	Val	Leu	Phe	Glu	Leu	Gly	Glu	Gly	Ser	Tyr	Phe	Ser	
490	gaa	ggg	gac	ggc	ttc	gcc	gag	gac	ccc	acc	atc	tcc	ctg	ctg	aca	ggc	1711
	Glu	Gly	Asp	Gly	Phe	Ala	Glu	Asp	Pro	Thr	Ile	Ser	Leu	Leu	Thr	Gly	
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	Ser	Glu	Pro	Pro	Lys	Ala	Lys	Asp	Pro	Thr	Val	Ser					
520	ggaggagctg	ggccagccgc	ccacccccac	ccccagtgc	gggctgggtct	tggggaggga											1817
	gggcagcctc	gcggtcttgg	gcactgggtgg	gtcggccgcc	atagccccag	taggacaaac											1877
	gggctcgggt	ctgggcagca	cctctgggtca	ggagggtcac	cctggcctgc	cagtctgcct											1937
	tcccccaacc	ccgtgtcctg	tggtttggtt	ggggcttcac	agccacacct	ggactgaccc											1997
	tgcaggttgt	tcatagtcag	aattgtattt	tggattttta	cacaactgtc	ccgttccccg											2057
	ctccacagag	atacacagat	atatacacac	agtgatgga	cggacaagac	aggcagagat											2117
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<210> SEQ ID NO 2

<211> LENGTH: 529

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 2

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Ala Phe Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp
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Ala Leu Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp
          35          40          45
Gln Gly Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn
          50          55          60
Asn Met Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys
          65          70          75          80
Val Val His Ile Glu Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp
          85          90          95
Thr Glu Phe Gln His Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu
          100          105          110
Glu Asn Ile Lys Arg Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu
          115          120          125
Asp Ile Lys Ile Arg Gln Asp Ser Val Thr Lys Leu Leu Thr Asp Val
          130          135          140
Gln Leu Met Lys Gly Lys Gln Glu Cys Met Asp Ser Lys Leu Leu Ala
          145          150          155          160
Met Lys His Glu Asn Glu Ala Leu Trp Arg Glu Val Ala Ser Leu Arg
          165          170          175
Gln Lys His Ala Gln Gln Gln Lys Val Val Asn Lys Leu Ile Gln Phe
          180          185          190
Leu Ile Ser Leu Val Gln Ser Asn Arg Ile Leu Gly Val Lys Arg Lys
          195          200          205
Ile Pro Leu Met Leu Asn Asp Ser Gly Ser Ala His Ser Met Pro Lys
          210          215          220
Tyr Ser Arg Gln Phe Ser Leu Glu His Val His Gly Ser Gly Pro Tyr
          225          230          235          240
Ser Ala Pro Ser Pro Ala Tyr Ser Ser Ser Ser Leu Tyr Ala Pro Asp
          245          250          255
Ala Val Ala Ser Ser Gly Pro Ile Ile Ser Asp Ile Thr Glu Leu Ala
          260          265          270
Pro Ala Ser Pro Met Ala Ser Pro Gly Gly Ser Ile Asp Glu Arg Pro
          275          280          285
Leu Ser Ser Ser Pro Leu Val Arg Val Lys Glu Glu Pro Pro Ser Pro
          290          295          300
Pro Gln Ser Pro Arg Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser
          305          310          315          320
Val Asp Thr Leu Leu Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg
          325          330          335
Glu Ser Glu Pro Ala Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg
          340          345          350
Gly His Thr Asp Thr Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser
          355          360          365
Thr Pro Glu Lys Cys Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu
          370          375          380
Ser Asp His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr
          385          390          395          400
Met Leu Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp
          405          410          415
Leu Phe Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu
          420          425          430
Asp Ser Ser Leu Ala Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro
          435          440          445
Pro Arg Pro Pro Glu Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln
          450          455          460

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Leu Val His Tyr Thr Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser
465 470 475 480
Val Asp Thr Gly Ser Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu
485 490 495
Gly Ser Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile
500 505 510
Ser Leu Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val
515 520 525
Ser

<210> SEQ ID NO 3

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A heat shock element. A nucleic acid molecule
that binds with a heat shock transcription factor
to stimulate gene expression

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)...(25)

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 3

ngaannttcn nnnnnnttcn ngaan

25